

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: November 28, 2001, 19:46:28 : Search time 19.5 Seconds
(without alignments)
406,338 Million cell updates/sec

Title: us-09-516-052-2_copy_28_177

Perfect score: 804
Sequence: 1 PEGUVMPLANVIRIMPKTL... YGVGMIDSMWMSGRVYON 150

Scoring table:

BLASTOM62
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues

Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match: 0%
Maximum Match: 100%

Listing list 45 summaries

Database:

A.Geneseq_0601:
1: /S1182/Arabidopsis thaliana/Geneseq/AA1981.DAT:
2: /S1182/Arabidopsis thaliana/Geneseq/AA1982.DAT:
3: /S1182/Arabidopsis thaliana/Geneseq/AA1983.DAT:
4: /S1182/Arabidopsis thaliana/Geneseq/AA1984.DAT:
5: /S1182/Arabidopsis thaliana/Geneseq/AA1985.DAT:
6: /S1182/Arabidopsis thaliana/Geneseq/AA1986.DAT:
7: /S1182/Arabidopsis thaliana/Geneseq/AA1987.DAT:
8: /S1182/Arabidopsis thaliana/Geneseq/AA1988.DAT:
9: /S1182/Arabidopsis thaliana/Geneseq/AA1989.DAT:
10: /S1182/Arabidopsis thaliana/Geneseq/AA1990.DAT:
11: /S1182/Arabidopsis thaliana/Geneseq/AA1991.DAT:
12: /S1182/Arabidopsis thaliana/Geneseq/AA1992.DAT:
13: /S1182/Arabidopsis thaliana/Geneseq/AA1993.DAT:
14: /S1182/Arabidopsis thaliana/Geneseq/AA1994.DAT:
15: /S1182/Arabidopsis thaliana/Geneseq/AA1995.DAT:
16: /S1182/Arabidopsis thaliana/Geneseq/AA1996.DAT:
17: /S1182/Arabidopsis thaliana/Geneseq/AA1997.DAT:
18: /S1182/Arabidopsis thaliana/Geneseq/AA1998.DAT:
19: /S1182/Arabidopsis thaliana/Geneseq/AA1999.DAT:
20: /S1182/Arabidopsis thaliana/Geneseq/AA2000.DAT:
21: /S1182/Arabidopsis thaliana/Geneseq/AA2001.DAT:
22: /S1182/Arabidopsis thaliana/Geneseq/AA2002.DAT:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	804	100.0	208	19	AAW71722 Arabidopsis leafy- Amino acid sequence
2	804	100.0	208	21	AAV54563 Soybean LEC1 # 1.
3	477	59.3	240	21	AAV62216 Soybean LEC1 # 2 p
4	476	59.2	355	21	AAV62224 Soybean LEC1 # 3.
5	476	59.2	373	21	AAV62225 Arabidopsis LEC1 c
6	476	59.1	90	21	AAV62217 Arabidopsis LEC1 # 3.
7	464	57.7	214	21	AAV6221 Arabidopsis LEC1 # 3.
8	458	57.0	171	21	AAV6221 Arabidopsis LEC1 # 3.
9	455.5	54.2	278	21	AAV6214 Arabidopsis LEC1 # 3.
10	426	53.0	146	21	AAV6215 Arabidopsis LEC1 # 3.
11	387.5	48.2	280	21	AAV6222 Wheat LEC1, trit

ALIGNMENTS

RESULT 1	
1	
AAW71722	standard; protein, 208 AA.
XX	
AC	AAW71722:
XX	
XX	11-JAN-1999 (first entry)
XX	
XX	Arabidopsis leafy-ecylophen 1 (L1F1) [11-JAN-1999]
XX	
XX	transgenic plant.
XX	
XX	Arabidopsis thaliana ecotype Wassilewskija.
XX	
XX	Key
XX	Binding-site 34..40
XX	note: "putative RNA binding site"
XX	61..72
XX	/note= "putative subunit interaction domain"
XX	
XX	W09837184-A1.
XX	
XX	27-AUG-1998.
XX	
XX	20-FEB-1998:
XX	98WD-US02998.
XX	
XX	19-FEB-1998:
XX	98US-0804534.
XX	
XX	21-FEB-1997:
XX	97US-0804534.
XX	
XX	(REGG) UNIV CALIFORNIA.
XX	
XX	Fischer RL, Goldberg RB, Harada JJ, Lohan T, Ohto M:

Pinus radiata tran
Arabidopsis thalia
Arabidopsis thalia
Arabidopsis thalia
N-YR. Homo sapi
Human prostate can
Pinus radiata tran
Arabidopsis thalia
Eucalyptus grandis
Pinus radiata tran
Arabidopsis thalia
Arabidopsis thalia
Mazze LEC1 # 3. %
Plant LEC1 consens
Eucalyptus grandis
Eucalyptus grandis
Arabidopsis thalia
Arabidopsis thalia
Zea mays protein t
Zea mays protein t
Pinus radiata tran
Zea mays protein t
Soybean trf1 protol
Arabidopsis thalia
Arabidopsis thalia
Human breast cance
Pinus radiata tran
Arabidopsis thalia
Human secreted pro
Arabidopsis thalia
Wheat trf1 protein
Mazze LEC1 # 3. %
Pinus radiata tran
Pinus radiata tran

XX WP1: 2000-076568/32.
 DR N-PSNR: AAA27456.

XX New HAP3 type CCAAT box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator, useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -

XX Claim 13; Page 82; 94pp; English.

XX The present sequence is the soybean leafy cotyledon 1 transcriptional
 CC activator, LEC1. This sequence is a HAP3-type CCAAT-box binding protein.
 CC LEC1 expression initiates the formation of embryo-like structures and
 CC improves growth and recovery of transformants. When apomixis occurs, i.e.
 CC the replacement of sexual reproduction by asexual reproduction, LEC1
 CC expression in the nucleolar intermedium, or cell specific expression in
 CC the megaspore mother cell would trigger embryo formation from maternal
 CC tissues only. This results in the production of seeds identical to the
 CC parent. Using LEC1, transgenic high yielding seeds could be developed. In
 CC addition, LEC1 could be used for positive selection of a transformed cell
 CC (transgenic plant), for increasing transformation efficiency and for
 CC increasing recovery of regenerated plants.

XX Sequence 240 AA;

Query Match 59.2%, Score 477, DB 21, Length 210;
 Host Local Similarity 66.0%, Pred. No. 1,70-45;
 Matches 95; Conservative 20; Mismatches 23; Indels 6; Gaps 3;

QY 1 REEDGYMIANVIEIMKELTPEHAKISDEAKELICEVEYESTVTSFANFENSDGPT 60
 DB 64 reqdltmplamvnlmklkllphkklshdketlqevseytstltggnctrrqfqrkl 123
 QY 61 ITADILIMAKSKLGFNNYVPLVETINPYETETPTGSAIAGPPPTROT-YGAGNIGH 119
 DB 124 ltaedylwamsklqtdytleptlmqthrycleqdr-lsmrgeplqtrvoayalata- 180
 QY 120 GPSHGLPPPGYGYGMIDQSMWG 143
 DB 181 ----vppthhnygtgaampg 202

RESULT 4

ID AAY96224 standard; Protein: 355 AA.

AC AAY96224;

DT 11-SEP-2000 (first entry)

DE Soybean LEC1 # 2 protein # 2.

KM Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KM selectable marker; transgenic plant; transgenic seed; HAP3.

OS Glycine max.

PN W0200028058-A2.

PU 18-MAY-2000.

TF 09-NOV-1999; *99W0-US26514.

PR 09-NOV-1998; 98US-0107643.

PR 10-NOV-1998; 98US-0107810.

PA (PIONEER) PIONEER HI-BRED INT INC.

PI Sun X. Hovster GJ. Gregory CA. Modimpalli R. Cabaco SL.

DR WP1: 2000-376568/32.
 TP N-PSNR: AAA27460.

XX New HAP3 type CCAAT box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator, useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -

XX Claim 13; Page 89-90; 94pp; English.

XX The present sequence is the soybean leafy cotyledon 1 transcriptional
 CC activator, LEC1. This sequence is a HAP3-type CCAAT-box binding protein.
 CC LEC1 expression initiates the formation of embryo-like structures and
 CC improves growth and recovery of transformants. When apomixis occurs,
 CC the replacement of sexual reproduction by asexual reproduction,
 CC the replacement of sexual reproduction by asexual reproduction, LEC1
 CC expression in the nucleolar intermedium, or cell specific expression
 CC in the megaspore mother cell would trigger embryo formation from
 CC maternal tissues only. This results in the production of seeds identical
 CC to the parent. Using LEC1, transgenic high yielding seeds could be
 CC developed. In addition, LEC1 could be used for positive selection of a
 CC transformed cell (transgenic plant), for increasing transformation
 CC efficiency and for increasing recovery of regenerated plants.
 CC Note: This sequence is different from that of AAY96220, even though
 CC they are both encoded by the same nucleotide sequence (AAA27460). The
 CC AAY96220 sequence has 18 stop codons distributed throughout the CDS,
 CC while the protein of AAY96224 has the stop codons omitted.

XX Sequence 355 AA;

Query Match 59.2%, Score 476, DB 21, Length 355;
 Host Local Similarity 66.0%, Pred. No. 3,80-45;
 Matches 95; Conservative 18; Mismatches 23; Indels 8; Gaps 5;

QY 1 REEDGYMIANVIEIMKELTPEHAKISDEAKELICEVEYESTVTSFANFENSDGPT 60
 DB 58 reqdltmplamvnlmklkllphkklshdketlqevseytstltggnctrrqfqrkl 117
 QY 61 ITADILIMAKSKLGFNNYVPLVETINPYETETPTGSAIAGPPPTROT-YGAGNIGH 119
 DB 118 ltaedylwamsklqtdytleptlmqthrycleqdr-lsmrgeplqtrvoayalata- 175
 QY 120 GPSHGLPPPGYGYGMIDQSMWG 143
 DB 176 ----vppthhnygtgaampg 194

RESULT 5

ID AAY96220 standard; Protein: 374 AA.

AC AAY96220;

DT 11-SEP-2000 (first entry)

DE Soybean LEC1 # 2 protein # 1.

KM Soybean; leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KM selectable marker; transgenic plant; transgenic seed; HAP3.

OS Glycine max.

PN W0200028058-A2.

PU 18-MAY-2000.

TF 09-NOV-1999; 99W0-US26514.

PR 09-NOV-1998; 98US-0107643.

PA (PIONEER) PIONEER HI-BRED INT INC.

PI Sun X. Hovster GJ. Gregory CA. Modimpalli R. Cabaco SL.

XX (PION) PIONEER HI-BRED INT INC.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 P1 LOAN KS, Golden-Korn W.L., Klein TM, Pasco-Gault S., Calhoun RB;
 P1 Sun X, Hester GJ, Gregory CA, Madipati R;
 XX WPI: 2000-37666732
 DR N-PSDB: AAA27457.
 XX
 PT New HMB3-type GCAT box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -
 PS
 PS Claim 13, page 83-84; 94pp; English.

CC The present sequence is the leafy cotyledon 1 transcriptional activator
 CC LEC1 of *Arabidopsis thaliana*. This sequence is a HAP1-type GCAT-box
 CC binding protein. LEC1 expression initiates the formation of embryonic
 CC structures and improves growth and recovery of transformed plants.
 CC apomixis is the replacement of sexual reproduction by asexual
 CC reproduction. LEC1 expression in the nucellus, integument, or cell
 CC specific expression in the megaspore mother cell triggers embryo
 CC formation from maternal tissues only. This results in the production of
 CC seeds identical to the parent using LEC1, transgenic high yielding seeds
 CC could be developed. In addition, LEC1 could be used for positive
 CC selection of a transformed cell (transgenic plant), for increasing
 CC transformation efficiency and for increasing recovery of regenerated
 CC plants.

XX Sequence 214 AA;

Query Match 57.7%; Score 464; DB 21; Length 214;
 Best Local Similarity 60.4%; Pred. No. 4.2e-44;
 Matches 93; Conservative 1c; Mismatches 21; Indels 24; Gaps 2;

QY 1 PEPQYMPANVIRIMPTLPSHAKISPAFTIQCSEYISFTVGEANEPCGQHQKT 60
 DB 48 regdlmpianvirimktlpphakisdakolqecvseystfvgandrcqeqkt 107
 QY 61 ITAERTIWMKSKIPPNVDPITVETINVEPTTFPFGALPSEHYRLDCTYGRSLTHIC 110
 DB 108 itaertlwmskltppnvdpitvettinvepttfpfgalpsahyrlasahfmas 167
 QY 111 YANNIGFHSPPS-----DELPPCP 130
 DB 168 fypatlmghthofitgpafigrlkapsasgspg 201

RESULT 8
 ID AAY96221 standard; Protein: 171 AA.
 XX
 AC AAY96221;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Soybean LEC1 # 3.
 XX
 KM Soybean leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KM selectable marker; transgenic plant; transgenic seed; HMB3.
 XX
 OS Glycine max.
 XX
 PN W0200028058-A2.
 XX
 PD 18-MAY-2000.
 XX
 PE 09-NOV-1999; 99W0-0526514.
 XX
 PR 09-NOV-1998; 980S-0107643.
 PR 10-NOV-1998; 980S-0107810.
 XX

XX (PION) PIONEER HI-BRED INT INC.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 XX
 P1 LOAN KS, Golden-Korn W.L., Klein TM, Pasco-Gault S., Calhoun RB;
 P1 Sun X, Hester GJ, Gregory CA, Madipati R;
 XX WPI: 2000-37666732
 DR N-PSDB: AAA27461.
 XX
 PT New HMB3-type GCAT box binding transcriptional activators,
 PT particularly leafy cotyledon 1 transcriptional activator useful for
 PT inducing somatic embryogenesis or apomixis in a plant cell -
 PS
 PS Claim 13, Page 91, 94pp; English.

CC The present sequence is the soybean leafy cotyledon 1 transcriptional
 CC activator, LEC1. This sequence is a HAP1-type GCAT-box binding protein.
 CC LEC1 expression initiates the formation of embryonic structures and
 CC improves growth and recovery of transformed plants. When apomixis occurs, i.e.,
 CC the replacement of sexual reproduction by asexual reproduction, LEC1
 CC expression in the nucellus, integument, or cell specific expression in
 CC the megaspore mother cell would trigger embryo formation from maternal
 CC tissues only. This results in the production of seeds identical to the
 CC parent. Using LEC1, transgenic high yielding seeds could be developed. In
 CC addition, LEC1 could be used for positive selection of a transformed cell
 CC (transgenic plant), for increasing transformation efficiency and for
 CC increasing recovery of regenerated plants.

XX Sequence 171 AA;

Query Match 57.0%; Score 458; DB 21; Length 171;
 Best Local Similarity 64.7%; Pred. No. 1.5e-43;
 Matches 95; Conservative 17; Mismatches 18; Indels 14; Gaps 3;

QY 1 PEPQYMPANVIRIMPTLPSHAKISPAFTIQCSEYISFTVGEANEPCGQHQKT 60
 DB 8 regdlmpianvirimktlpphakisdakolqecvseystfvaenecqeqkt 67
 QY 61 ITAERTIWMKSKIPPNVDPITVETINVEPTTFPFGALPSEHYRLDCTYGRSLTHIC 120
 DB 68 itaertlwmskltppnvdpitvettinvepttfpfgalpsahyrlasahfmas 116
 QY 121 PSHGLPP--CPYGYGMD 137
 DB 117 nmahpylshatgmd 144

RESULT 9
 ID AAY96214 standard; Protein: 278 AA.
 XX
 AC AAY96214;
 XX
 DT 11-SEP-2000 (first entry)
 XX
 DE Maize LEC1 # 1.
 XX
 KM Maize leafy cotyledon 1 transcriptional activator; LEC1; apomixis;
 KM selectable marker; transgenic plant; transgenic seed; HMB3.
 XX
 OS Zea mays.
 XX
 PN W0200028058-A2.
 XX
 PD 18-MAY-2000.
 XX
 PE 09-NOV-1999; 99W0-0526514.
 XX
 PR 09-NOV-1998; 980S-0107643.
 PR 10-NOV-1998; 980S-0107810.
 XX

[illegible][illegible]

